

## SEQUENCE LISTING

&lt;110&gt; Hart, Derek N J

<120> Enzyme having S-adenosyl-L-homocysteine hydrolase  
(AHCY) type activity

&lt;130&gt; 24305 MRB

&lt;140&gt; JP 516412/98

&lt;141&gt; 1999-05-19

&lt;150&gt; PCT/NZ97/00133

&lt;151&gt; 1997-10-06

&lt;150&gt; NZ 299507

&lt;151&gt; 1996-10-04

&lt;160&gt; 2

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 2563

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (3)..(1847)

<223> Open reading frame extends without a stop codon  
for the full 5' nucleotide sequence. The  
initiation codon has yet to be identified.

&lt;400&gt; 1

gg	cgc	ggg	cag	gtc	gga	gct	cgg	agc	tgc	tgc	ttc	tgg	ttc	tct	tgt	47
	Arg	Gly	Gln	Val	Gly	Ala	Arg	Ser	Cys	Cys	Phe	Trp	Phe	Ser	Cys	
	1				5				10					15		

ggc	cac	cgt	cgc	tgt	ccg	gct	gcc	ttg	ggc	tgc	cga	aca	gac	aag	gcg	95
Gly	His	Arg	Arg	Cys	Pro	Ala	Ala	Leu	Gly	Cys	Arg	Thr	Asp	Lys	Ala	
				20				25						30		

tgg	gcc	aca	gca	cct	cag	aag	ccg	acg	cag	ctc	gac	gca	ggg	gcc	ggc	143
Trp	Ala	Thr	Ala	Pro	Gln	Lys	Pro	Thr	Gln	Leu	Asp	Ala	Gly	Ala	Gly	
				35				40					45			

agg	agg	gtg	ggc	gat	cgc	gtg	tcg	gag	ggc	gcc	gcg	cgg	gca	ggc	ggg	191
Arg	Arg	Val	Gly	Asp	Arg	Val	Ser	Glu	Gly	Ala	Ala	Arg	Ala	Gly	Gly	
		50					55					60				

cgg	gcg	cca	gag	ggg	gaa	aga	ggc	ggg	ggc	ggc	ggg	tca	gcc	gct	ggc	239
Arg	Ala	Pro	Glu	Gly	Glu	Arg	Gly	Gly	Gly	Gly	Gly	Ser	Ala	Ala	Gly	
	65					70					75					

cgg	gcc	ggc	ggg	gga	atg	tcg	atg	cct	gac	gcg	atg	ccg	ctg	ccc	ggg	287
Arg	Ala	Gly	Gly	Gly	Met	Ser	Met	Pro	Asp	Ala	Met	Pro	Leu	Pro	Gly	
	80				85				90					95		

gtc	ggg	gag	gag	ctg	aag	cag	gcc	aag	gag	atc	gag	gac	gcc	gag	aag	335
Val	Gly	Glu	Glu	Leu	Lys	Gln	Ala	Lys	Glu	Ile	Glu	Asp	Ala	Glu	Lys	





gct	ggg	aag	ctc	tgt	gtt	ccg	gcc	atg	aac	gtc	aat	gat	tct	gtt	acc	1103
Ala	Gly	Lys	Leu	Cys	Val	Pro	Ala	Met	Asn	Val	Asn	Asp	Ser	Val	Thr	
			355					360					365			
aaa	cag	aag	ttt	gat	aac	ttg	tac	tgc	tgc	cga	gaa	tcc	att	ttg	gat	1151
Lys	Gln	Lys	Phe	Asp	Asn	Leu	Tyr	Cys	Cys	Arg	Glu	Ser	Ile	Leu	Asp	
		370					375					380				
ggc	ctg	aag	agg	acc	aca	gat	gtg	atg	ttt	ggg	ggg	aaa	caa	gtg	gtg	1199
Gly	Leu	Lys	Arg	Thr	Thr	Asp	Val	Met	Phe	Gly	Gly	Lys	Gln	Val	Val	
	385					390					395					
gtg	tgt	ggc	tat	ggg	gag	gta	ggc	aag	ggc	tgc	tgt	gct	gct	ctc	aaa	1247
Val	Cys	Gly	Tyr	Gly	Glu	Val	Gly	Lys	Gly	Cys	Cys	Ala	Ala	Leu	Lys	
400					405				410						415	
gct	ctt	gga	gca	att	gtc	tac	att	acc	gaa	atc	gac	ccc	atc	tgt	gct	1295
Ala	Leu	Gly	Ala	Ile	Val	Tyr	Ile	Thr	Glu	Ile	Asp	Pro	Ile	Cys	Ala	
				420					425					430		
ctg	cag	gcc	tgc	atg	gat	ggg	ttc	agg	gtg	gta	aag	cta	aat	gaa	gtc	1343
Leu	Gln	Ala	Cys	Met	Asp	Gly	Phe	Arg	Val	Val	Lys	Leu	Asn	Glu	Val	
			435					440					445			
atc	cgg	caa	gtc	gat	gtc	gta	ata	act	tgc	aca	gga	aat	aag	aat	gta	1391
Ile	Arg	Gln	Val	Asp	Val	Val	Ile	Thr	Cys	Thr	Gly	Asn	Lys	Asn	Val	
		450					455					460				
gtg	aca	cgg	gag	cac	ttg	gat	cgc	atg	aaa	aac	agt	tgt	atc	gta	tgc	1439
Val	Thr	Arg	Glu	His	Leu	Asp	Arg	Met	Lys	Asn	Ser	Cys	Ile	Val	Cys	
	465					470					475					
aat	atg	ggc	cac	tcc	aac	aca	gaa	atc	gat	gtg	acc	agc	ctc	cgc	act	1487
Asn	Met	Gly	His	Ser	Asn	Thr	Glu	Ile	Asp	Val	Thr	Ser	Leu	Arg	Thr	
480					485				490						495	
ccg	gag	ctg	acg	tgg	gag	cga	gta	cgt	tct	cag	gtg	gac	cat	gtc	atc	1535
Pro	Glu	Leu	Thr	Trp	Glu	Arg	Val	Arg	Ser	Gln	Val	Asp	His	Val	Ile	
			500						505					510		
tgg	cca	gat	ggc	aaa	cga	gtt	gtc	ctc	ctg	gca	gag	ggg	cgt	cta	ctc	1583
Trp	Pro	Asp	Gly	Lys	Arg	Val	Val	Leu	Leu	Ala	Glu	Gly	Arg	Leu	Leu	
			515					520					525			
aat	ttg	agc	tgc	tcc	aca	gtt	ccc	acc	ttt	gtt	ctg	tcc	atc	aca	gcc	1631
Asn	Leu	Ser	Cys	Ser	Thr	Val	Pro	Thr	Phe	Val	Leu	Ser	Ile	Thr	Ala	
		530					535					540				
aca	aca	cag	gct	ttg	gca	ctg	ata	gaa	ctc	tat	aat	gca	ccc	gag	ggg	1679
Thr	Thr	Gln	Ala	Leu	Ala	Leu	Ile	Glu	Leu	Tyr	Asn	Ala	Pro	Glu	Gly	
	545					550					555					
cga	tac	aag	cag	gat	gtg	tac	ttg	ctt	cct	aag	aaa	atg	gat	gaa	tac	1727
Arg	Tyr	Lys	Gln	Asp	Val	Tyr	Leu	Leu	Pro	Lys	Lys	Met	Asp	Glu	Tyr	
560					565				570						575	
gtt	gcc	agc	ttg	cat	ctg	cca	tca	ttt	gat	gcc	cac	ctt	aca	gag	ctg	1775
Val	Ala	Ser	Leu	His	Leu	Pro	Ser	Phe	Asp	Ala	His	Leu	Thr	Glu	Leu	
			580						585					590		

aca gat gac caa gca aaa tat ctg gga ctc aac aaa aat ggg cca ttc 1823  
 Thr Asp Asp Gln Ala Lys Tyr Leu Gly Leu Asn Lys Asn Gly Pro Phe  
 595 600 605

aaa cct aat tat tac aga tac taa tggaccatac taccaaggac cagtccacct 1877  
 Lys Pro Asn Tyr Tyr Arg Tyr  
 610 615

gaaccacaca ctctaaagaa atatttttta agataacttt tattttcttc ttactccttt 1937  
 cctcttgatt tttttcctat aatttcattc ttgttttttc atctcattat ccaagttctg 1997  
 cagaccacac aggaacttgc ttcattggctc tttagatgaa atagaagttc agggtccttc 2057  
 actctagtca ctaaagaagg attttactcc cccagcccag aaagggtgatt cttctcttta 2117  
 ccatttctgg ggacttttagt cttaattagg taccttatta acaggaaatg ctaaggtacc 2177  
 ttctctgtgg aacaatctgc aatgtctaaa tcgccttaaa agagcccatt tcttagctgc 2237  
 tgaaatcagt gctctttcac ttcttcagag aagcagggat ggtacctacc cggcaggtag 2297  
 gttagatgtg ggtgggtgcat gttaatttcc cttagaagtt ccaagccctg tttcctgcgt 2357  
 aaagggtggtg tgtccagttc agagatgtgt ataatgagca tggcttggtta agatcaggag 2417  
 gccacttgg atttatagta tagcccttcc tccactccca ccagacttgc tcatttttctg 2477  
 agtttttaac tagactacac tctatttgag ttttaatttg tcctctagga tttatttctg 2537  
 ttgtccaaaa aaaaaaaaaa aaaaaa 2563

<210> 2  
 <211> 614  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 Arg Gly Gln Val Gly Ala Arg Ser Cys Cys Phe Trp Phe Ser Cys Gly  
 1 5 10 15  
 His Arg Arg Cys Pro Ala Ala Leu Gly Cys Arg Thr Asp Lys Ala Trp  
 20 25 30  
 Ala Thr Ala Pro Gln Lys Pro Thr Gln Leu Asp Ala Gly Ala Gly Arg  
 35 40 45  
 Arg Val Gly Asp Arg Val Ser Glu Gly Ala Ala Arg Ala Gly Gly Arg  
 50 55 60  
 Ala Pro Glu Gly Glu Arg Gly Gly Gly Gly Gly Ser Ala Ala Gly Arg  
 65 70 75 80  
 Ala Gly Gly Gly Met Ser Met Pro Asp Ala Met Pro Leu Pro Gly Val  
 85 90 95

Gly Glu Glu Leu Lys Gln Ala Lys Glu Ile Glu Asp Ala Glu Lys Tyr  
 100 105 110

Ser Phe Met Ala Thr Val Thr Lys Ala Pro Lys Lys Gln Ile Gln Phe

115		120		125
Ala Asp Asp Met Gln Glu Phe Thr Lys Phe Pro Thr Lys Thr Gly Arg				
130		135		140
Arg Ser Leu Ser Arg Ser Ile Ser Gln Ser Ser Thr Asp Ser Tyr Ser				
145		150		155
Ser Ala Ala Ser Tyr Thr Asp Ser Ser Asp Asp Glu Val Ser Pro Arg				
		165		170
Glu Lys Gln Gln Thr Asn Ser Lys Gly Ser Ser Asn Phe Cys Val Lys				
		180		185
Asn Ile Lys Gln Ala Glu Phe Gly Arg Arg Glu Ile Glu Ile Ala Glu				
		195		200
Gln Asp Met Ser Ala Leu Ile Ser Leu Arg Lys Arg Ala Gln Gly Glu				
		210		215
Lys Pro Leu Ala Gly Ala Lys Ile Val Gly Cys Thr His Ile Thr Ala				
225		230		235
Gln Thr Ala Val Leu Ile Glu Thr Leu Cys Ala Leu Gly Ala Gln Cys				
		245		250
Arg Trp Ser Ala Cys Asn Ile Tyr Ser Thr Gln Asn Glu Val Ala Ala				
		260		265
Ala Leu Ala Glu Ala Gly Val Ala Val Phe Ala Trp Lys Gly Glu Ser				
		275		280
Glu Asp Asp Phe Trp Trp Cys Ile Asp Arg Cys Val Asn Met Asp Gly				
		290		295
Trp Gln Ala Asn Met Ile Leu Asp Asp Gly Gly Asp Leu Thr His Trp				
305		310		315
Val Tyr Lys Lys Tyr Pro Asn Val Phe Lys Lys Ile Arg Gly Ile Val				
		325		330
Glu Glu Ser Val Thr Gly Val His Arg Leu Tyr Gln Leu Ser Lys Ala				
		340		345
Gly Lys Leu Cys Val Pro Ala Met Asn Val Asn Asp Ser Val Thr Lys				
		355		360
Gln Lys Phe Asp Asn Leu Tyr Cys Cys Arg Glu Ser Ile Leu Asp Gly				
		370		375
Leu Lys Arg Thr Thr Asp Val Met Phe Gly Gly Lys Gln Val Val Val				
385		390		395
Cys Gly Tyr Gly Glu Val Gly Lys Gly Cys Cys Ala Ala Leu Lys Ala				
		405		410
Leu Gly Ala Ile Val Tyr Ile Thr Glu Ile Asp Pro Ile Cys Ala Leu				
		420		425
Gln Ala Cys Met Asp Gly Phe Arg Val Val Lys Leu Asn Glu Val Ile				
		435		440
				445

Arg	Gln	Val	Asp	Val	Val	Ile	Thr	Cys	Thr	Gly	Asn	Lys	Asn	Val	Val	450	455	460	
Thr	Arg	Glu	His	Leu	Asp	Arg	Met	Lys	Asn	Ser	Cys	Ile	Val	Cys	Asn	465	470	475	480
Met	Gly	His	Ser	Asn	Thr	Glu	Ile	Asp	Val	Thr	Ser	Leu	Arg	Thr	Pro		485	490	495
Glu	Leu	Thr	Trp	Glu	Arg	Val	Arg	Ser	Gln	Val	Asp	His	Val	Ile	Trp		500	505	510
Pro	Asp	Gly	Lys	Arg	Val	Val	Leu	Leu	Ala	Glu	Gly	Arg	Leu	Leu	Asn		515	520	525
Leu	Ser	Cys	Ser	Thr	Val	Pro	Thr	Phe	Val	Leu	Ser	Ile	Thr	Ala	Thr		530	535	540
Thr	Gln	Ala	Leu	Ala	Leu	Ile	Glu	Leu	Tyr	Asn	Ala	Pro	Glu	Gly	Arg	545	550	555	560
Tyr	Lys	Gln	Asp	Val	Tyr	Leu	Leu	Pro	Lys	Lys	Met	Asp	Glu	Tyr	Val		565	570	575
Ala	Ser	Leu	His	Leu	Pro	Ser	Phe	Asp	Ala	His	Leu	Thr	Glu	Leu	Thr		580	585	590
Asp	Asp	Gln	Ala	Lys	Tyr	Leu	Gly	Leu	Asn	Lys	Asn	Gly	Pro	Phe	Lys	595	600	605	
Pro	Asn	Tyr	Tyr	Arg	Tyr											610			